

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/567/282
Source: IFWP
Date Processed by STIC: 2/13/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 02/13/2006

PATENT APPLICATION: US/10/567,282

TIME: 12:47:48

Input Set : E:\9301-237-999.txt

Output Set: N:\CRF4\02132006\J567282.raw

4 <110> APPLICANT: Schadt, Eric E.
 5 Monks, Stephanie A.
 7 <120> TITLE OF INVENTION: COMPUTER SYSTEMS AND METHODS FOR
 8 INFERRING CASUALITY FROM CELLULAR CONSTITUENT ABUNDANCE DATA
 11 <130> FILE REFERENCE: 9301-237-228
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/567,282
 C--> 14 <141> CURRENT FILING DATE: 2006-02-03
 16 <150> PRIOR APPLICATION NUMBER: 60/575,499
 17 <151> PRIOR FILING DATE: 2004-05-28
 19 <150> PRIOR APPLICATION NUMBER: 60/497,470
 20 <151> PRIOR FILING DATE: 2003-08-21
 22 <150> PRIOR APPLICATION NUMBER: 60/492,682
 23 <151> PRIOR FILING DATE: 2003-08-05
 25 <160> NUMBER OF SEQ ID NOS: 24
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 572
 31 <212> TYPE: PRT
 32 <213> ORGANISM: homo sapiens polypeptide
 34 <220> FEATURE:
 35 <223> OTHER INFORMATION: malic enzyme ME1
 37 <400> SEQUENCE: 1
 38 Met Glu Pro Glu Ala Pro Arg Arg Arg His Thr His Gln Arg Gly Tyr
 39 1 5 10 15
 40 Leu Leu Thr Arg Asn Pro His Leu Asn Lys Asp Leu Ala Phe Thr Leu
 41 20 25 30
 42 Glu Glu Arg Gln Gln Leu Asn Ile His Gly Leu Leu Pro Pro Ser Phe
 43 35 40 45
 44 Asn Ser Gln Glu Ile Gln Val Leu Arg Val Val Lys Asn Phe Glu His
 45 50 55 60
 46 Leu Asn Ser Asp Phe Asp Arg Tyr Leu Leu Leu Met Asp Leu Gln Asp
 47 65 70 75 80
 48 Arg Asn Glu Lys Leu Phe Tyr Arg Val Leu Thr Ser Asp Ile Glu Lys
 49 85 90 95
 50 Phe Met Pro Ile Val Tyr Thr Pro Thr Val Gly Leu Ala Cys Gln Gln
 51 100 105 110
 52 Tyr Ser Leu Val Phe Arg Lys Pro Arg Gly Leu Phe Ile Thr Ile His
 53 115 120 125
 54 Asp Arg Gly His Ile Ala Ser Val Leu Asn Ala Trp Pro Glu Asp Val
 55 130 135 140
 56 Ile Lys Ala Ile Val Val Thr Asp Gly Glu Arg Ile Leu Gly Leu Gly
 57 145 150 155 160
 58 Asp Leu Gly Cys Asn Gly Met Gly Ile Pro Val Gly Lys Leu Ala Leu

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59				165				170				175				
60	Tyr	Thr	Ala	Cys	Gly	Gly	Met	Asn	Pro	Gln	Glu	Cys	Leu	Pro	Val	Ile
61				180				185					190			
62	Leu	Asp	Val	Gly	Thr	Glu	Asn	Glu	Glu	Leu	Leu	Lys	Asp	Pro	Leu	Tyr
63			195					200					205			
64	Ile	Gly	Leu	Arg	Gln	Arg	Arg	Val	Arg	Gly	Ser	Glu	Tyr	Asp	Asp	Phe
65		210					215					220				
66	Leu	Asp	Glu	Phe	Met	Glu	Ala	Val	Ser	Ser	Lys	Tyr	Gly	Met	Asn	Cys
67	225					230					235				240	
68	Leu	Ile	Gln	Phe	Glu	Asp	Phe	Ala	Asn	Val	Asn	Ala	Phe	Arg	Leu	Leu
69				245				250						255		
70	Asn	Lys	Tyr	Arg	Asn	Gln	Tyr	Cys	Thr	Phe	Asn	Asp	Asp	Ile	Gln	Gly
71			260					265						270		
72	Thr	Ala	Ser	Val	Ala	Val	Ala	Gly	Leu	Leu	Ala	Ala	Leu	Arg	Ile	Thr
73			275					280					285			
74	Lys	Asn	Lys	Leu	Ser	Asp	Gln	Thr	Ile	Leu	Phe	Gln	Gly	Ala	Gly	Glu
75		290				295						300				
76	Ala	Ala	Leu	Gly	Ile	Ala	His	Leu	Ile	Val	Met	Ala	Leu	Glu	Lys	Glu
77	305					310					315				320	
78	Gly	Leu	Pro	Lys	Glu	Lys	Ala	Ile	Lys	Lys	Ile	Trp	Leu	Val	Asp	Ser
79				325						330					335	
80	Lys	Gly	Leu	Ile	Val	Lys	Gly	Arg	Ala	Ser	Leu	Thr	Gln	Glu	Lys	Glu
81			340					345						350		
82	Lys	Phe	Ala	His	Glu	His	Glu	Glu	Met	Lys	Asn	Leu	Glu	Ala	Ile	Val
83			355					360					365			
84	Gln	Glu	Ile	Lys	Pro	Thr	Ala	Leu	Ile	Gly	Val	Ala	Ala	Ile	Gly	Gly
85		370					375					380				
86	Ala	Phe	Ser	Glu	Gln	Ile	Leu	Lys	Asp	Met	Ala	Ala	Phe	Asn	Glu	Arg
87	385					390					395				400	
88	Pro	Ile	Ile	Phe	Ala	Leu	Ser	Asn	Pro	Thr	Ser	Lys	Ala	Glu	Cys	Ser
89				405						410					415	
90	Ala	Glu	Gln	Cys	Tyr	Lys	Ile	Thr	Lys	Gly	Arg	Ala	Ile	Phe	Ala	Ser
91			420						425					430		
92	Gly	Ser	Pro	Phe	Asp	Pro	Val	Thr	Leu	Pro	Asn	Gly	Gln	Thr	Leu	Tyr
93			435					440					445			
94	Pro	Gly	Gln	Gly	Asn	Asn	Ser	Tyr	Val	Phe	Pro	Gly	Val	Ala	Leu	Gly
95		450					455					460				
96	Val	Val	Ala	Cys	Gly	Leu	Arg	Gln	Ile	Thr	Asp	Asn	Ile	Phe	Leu	Thr
97	465					470					475				480	
98	Thr	Ala	Glu	Val	Ile	Ala	Gln	Gln	Val	Ser	Asp	Lys	His	Leu	Glu	Glu
99				485						490					495	
100	Gly	Arg	Leu	Tyr	Pro	Pro	Leu	Asn	Thr	Ile	Arg	Asp	Val	Ser	Leu	Lys
101				500						505				510		
102	Ile	Ala	Glu	Lys	Ile	Val	Lys	Asp	Ala	Tyr	Gln	Glu	Lys	Thr	Ala	Thr
103			515						520					525		
104	Val	Tyr	Pro	Glu	Pro	Gln	Asn	Lys	Glu	Ala	Phe	Val	Arg	Ser	Gln	Met
105		530					535					540				
106	Tyr	Ser	Thr	Asp	Tyr	Asp	Gln	Ile	Leu	Pro	Asp	Cys	Tyr	Ser	Trp	Pro
107	545					550					555				560	

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```

108 Glu Glu Val Gln Lys Ile Gln Thr Lys Val Asp Gln
109                      565                      570
112 <210> SEQ ID NO: 2
113 <211> LENGTH: 572
114 <212> TYPE: PRT
115 <213> ORGANISM: mus musculus polypeptide
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Mod1
120 <400> SEQUENCE: 2
121 Met Glu Pro Arg Ala Pro Arg Arg Arg His Thr His Gln Arg Gly Tyr
122 1                      5                      10                      15
123 Leu Leu Thr Arg Asp Pro His Leu Asn Lys Asp Leu Ala Phe Thr Leu
124                      20                      25                      30
125 Glu Glu Arg Gln Gln Leu Asn Ile His Gly Leu Leu Pro Pro Cys Ile
126                      35                      40                      45
127 Ile Ser Gln Glu Leu Gln Val Leu Arg Ile Ile Lys Asn Phe Glu Arg
128 50                      55                      60
129 Leu Asn Ser Asp Phe Asp Arg Tyr Leu Leu Leu Met Asp Leu Gln Asp
130 65                      70                      75                      80
131 Arg Asn Glu Lys Leu Phe Tyr Ser Val Leu Met Ser Asp Val Glu Lys
132                      85                      90                      95
133 Phe Met Pro Ile Val Tyr Thr Pro Thr Val Gly Leu Ala Cys Gln Gln
134                      100                     105                     110
135 Tyr Ser Leu Ala Phe Arg Lys Pro Arg Gly Leu Phe Ile Ser Ile His
136                      115                     120                     125
137 Asp Lys Gly His Ile Ala Ser Val Leu Asn Ala Trp Pro Glu Asp Val
138                      130                     135                     140
139 Val Lys Ala Ile Val Val Thr Asp Gly Glu Arg Ile Leu Gly Leu Gly
140 145                     150                     155                     160
141 Asp Leu Gly Cys Asn Gly Met Gly Ile Pro Val Gly Lys Leu Ala Leu
142                      165                     170                     175
143 Tyr Thr Ala Cys Gly Gly Val Asn Pro Gln Gln Cys Leu Pro Ile Thr
144                      180                     185                     190
145 Leu Asp Val Gly Thr Glu Asn Glu Glu Leu Leu Lys Asp Pro Leu Tyr
146                      195                     200                     205
147 Ile Gly Leu Arg His Arg Arg Val Arg Gly Pro Glu Tyr Asp Ala Phe
148                      210                     215                     220
149 Leu Asp Glu Phe Met Glu Ala Ala Ser Ser Lys Tyr Gly Met Asn Cys
150 225                     230                     235                     240
151 Leu Ile Gln Phe Glu Asp Phe Ala Asn Arg Asn Ala Phe Arg Leu Leu
152                      245                     250                     255
153 Asn Lys Tyr Arg Asn Lys Tyr Cys Thr Phe Asn Asp Asp Ile Gln Gly
154                      260                     265                     270
155 Thr Ala Ser Val Ala Val Ala Gly Leu Leu Ala Ala Leu Arg Ile Thr
156                      275                     280                     285
157 Lys Asn Lys Leu Ser Asp Gln Thr Val Leu Phe Gln Gly Ala Gly Glu
158                      290                     295                     300
159 Ala Ala Leu Gly Ile Ala His Leu Val Val Met Ala Met Glu Lys Glu
160 305                     310                     315                     320

```

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```

161 Gly Leu Ser Lys Glu Asn Ala Arg Lys Lys Ile Trp Leu Val Asp Ser
162           325           330           335
163 Lys Gly Leu Ile Val Lys Gly Arg Ala Ser Leu Thr Glu Glu Lys Glu
164           340           345           350
165 Val Phe Ala His Glu His Glu Glu Met Lys Asn Leu Glu Ala Ile Val
166           355           360           365
167 Gln Lys Ile Lys Pro Thr Ala Leu Ile Gly Val Ala Ala Ile Gly Gly
168           370           375           380
169 Ala Phe Thr Glu Gln Ile Leu Lys Asp Met Ala Ala Phe Asn Glu Arg
170 385           390           395           400
171 Pro Ile Ile Phe Ala Leu Ser Ser Pro Thr Ser Lys Ala Glu Cys Ser
172           405           410           415
173 Ala Asp Glu Cys Tyr Lys Val Thr Lys Gly Arg Ala Ile Phe Ala Ser
174           420           425           430
175 Gly Ser Pro Phe Asp Pro Val Thr Leu Pro Asp Gly Arg Thr Leu Phe
176           435           440           445
177 Pro Gly Gln Gly Asn Asn Ser Tyr Val Phe Pro Gly Val Ala Leu Gly
178           450           455           460
179 Val Val Ala Cys Gly Leu Arg His Ile Asp Asp Lys Val Phe Leu Thr
180 465           470           475           480
181 Thr Arg Glu Val Ile Ser Gln Gln Val Ser Asp Lys His Leu Gln Glu
182           485           490           495
183 Gly Arg Leu Tyr Pro Pro Leu Asn Thr Ile Arg Gly Val Ser Leu Lys
184           500           505           510
185 Ile Ala Val Lys Ile Val Gln Asp Ala Tyr Lys Glu Lys Met Ala Thr
186           515           520           525
187 Val Tyr Pro Glu Pro Gln Asn Lys Glu Glu Phe Val Ser Ser Gln Met
188           530           535           540
189 Tyr Ser Thr Asn Tyr Asp Gln Ile Leu Pro Asp Cys Tyr Pro Trp Pro
190 545           550           555           560
191 Ala Glu Val Gln Lys Ile Gln Thr Lys Val Asn Gln
192           565           570

```

195 <210> SEQ ID NO: 3

196 <211> LENGTH: 564

197 <212> TYPE: PRT

198 <213> ORGANISM: homo sapiens polypeptide - ME3

200 <220> FEATURE:

201 <221> NAME/KEY: VARIANT

202 <222> LOCATION: 9, 18, 27, 55, 66, 88, 157, 199, 219, 305, 307, 323, 387,
203 519

204 <223> OTHER INFORMATION: Xaa = Any Amino Acid

206 <400> SEQUENCE: 3

```

W--> 207 Ile Lys Glu Lys Gly Lys Pro Leu Xaa Leu Asn Pro Arg Thr Asn Lys
208 1           5           10           15
W--> 209 Gly Xaa Ala Phe Thr Leu Gln Glu Arg Gln Xaa Leu Gly Leu Gln Gly
210           20           25           30
211 Leu Leu Pro Pro Lys Ile Glu Thr Gln Asp Ile Gln Ala Leu Arg Phe
212           35           40           45
W--> 213 His Arg Asn Leu Lys Lys Xaa Thr Ser Pro Leu Glu Lys Tyr Ile Tyr

```

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```

      214      50      55      60
W--> 215 Ile Xaa Gly Ile Gln Glu Arg Asn Glu Lys Leu Phe Tyr Arg Ile Leu
      216 65      70      75      80
W--> 217 Gln Asp Asp Ile Glu Ser Leu Xaa Pro Ile Val Tyr Thr Pro Thr Val
      218      85      90      95
      219 Gly Leu Ala Cys Ser Gln Tyr Gly His Ile Phe Arg Arg Pro Lys Gly
      220      100      105      110
      221 Leu Phe Ile Ser Ile Ser Asp Arg Gly His Val Arg Ser Ile Val Asp
      222      115      120      125
      223 Asn Trp Pro Glu Asn His Val Lys Ala Val Val Val Thr Asp Gly Glu
      224      130      135      140
W--> 225 Arg Ile Leu Gly Leu Gly Asp Leu Gly Val Tyr Gly Xaa Gly Ile Pro
      226 145      150      155      160
      227 Val Gly Lys Leu Cys Leu Tyr Thr Ala Cys Ala Gly Ile Arg Pro Asp
      228      165      170      175
      229 Arg Cys Leu Pro Val Cys Ile Asp Val Gly Thr Asp Asn Ile Ala Leu
      230      180      185      190
W--> 231 Leu Lys Asp Pro Phe Tyr Xaa Gly Leu Tyr Gln Lys Arg Asp Arg Thr
      232      195      200      205
W--> 233 Gln Gln Tyr Asp Asp Leu Ile Asp Glu Phe Xaa Lys Ala Ile Thr Asp
      234      210      215      220
      235 Arg Tyr Gly Arg Asn Thr Leu Ile Gln Phe Glu Asp Phe Gly Asn His
      236 225      230      235      240
      237 Asn Ala Phe Arg Phe Leu Arg Lys Tyr Arg Glu Lys Tyr Cys Thr Phe
      238      245      250      255
      239 Asn Asp Asp Ile Gln Gly Thr Ala Ala Val Ala Leu Ala Gly Leu Leu
      240      260      265      270
      241 Ala Ala Gln Lys Val Ile Ser Lys Pro Ile Ser Glu His Lys Ile Leu
      242      275      280      285
      243 Phe Leu Gly Ala Gly Glu Ala Ala Leu Gly Ile Ala Asn Leu Ile Val
      244      290      295      300
W--> 245 Xaa Ser Xaa Val Glu Asn Gly Leu Ser Glu Gln Glu Ala Gln Lys Lys
      246 305      310      315      320
W--> 247 Ile Trp Xaa Phe Asp Lys Tyr Gly Leu Leu Val Lys Gly Arg Lys Ala
      248      325      330      335
      249 Lys Ile Asp Ser Tyr Gln Glu Pro Phe Thr His Ser Ala Pro Glu Ser
      250      340      345      350
      251 Ile Pro Asp Thr Phe Glu Asp Ala Val Asn Ile Leu Lys Pro Ser Thr
      252      355      360      365
      253 Ile Ile Gly Val Ala Gly Ala Gly Arg Leu Phe Thr Pro Asp Val Ile
      254      370      375      380
W--> 255 Arg Ala Xaa Ala Ser Ile Asn Glu Arg Pro Val Ile Phe Ala Leu Ser
      256 385      390      395      400
      257 Asn Pro Thr Ala Gln Ala Glu Cys Thr Ala Glu Glu Ala Tyr Thr Leu
      258      405      410      415
      259 Thr Glu Gly Arg Cys Leu Phe Ala Ser Gly Ser Pro Phe Gly Pro Val
      260      420      425      430
      261 Lys Leu Thr Asp Gly Arg Val Phe Thr Pro Gly Gln Gly Asn Asn Val
      262      435      440      445

```

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 9,18,27,55,66,88,157,199,219,305,307,323,387,519
Seq#:18; N Pos. 7,8

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:5; Line(s) 372
Seq#:6; Line(s) 396

VERIFICATION SUMMARY

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Output Set: N:\CRF4\02132006\J567282.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:16
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:48
L:215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:64
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:80
L:225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:144
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:192
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:208
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:304
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:320
L:255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:384
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:512
L:970 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0